AMENDMENTS TO THE CLAIMS

1. (Currently Amended) A method for diagnosing cancer, comprising the detection of a methylated SPARC nucleic acid molecule or a variant thereof in a sample from a subject, wherein the methylated SPARC nucleic acid molecule comprises a sequence corresponding to the nucleic acid sequence set forth in SEQ ID NO: 1 (Figure 6).

2. (Original) The method of claim 1 wherein the presence of a methylated SPARC nucleic acid molecule is compared to a sample from a subject without cancer.

3. (Original) The method of claim 1 wherein the sample is obtained from a mammal suspected of having a proliferative cell growth disorder.

4. (Original) The method of claim 1 wherein the sample is obtained from a mammal suspected of having a pancreatic cancer.

5. (Cancelled)

6. (Previously Presented) The method of claim 1, wherein a methylated SPARC nucleic acid molecule comprises a sequence having at least about 80% sequence identity to a molecule identified in SEQ ID NO: 1 (Figure 6).

7. (Previously Presented) The method of claim 1, wherein a methylated SPARC nucleic acid molecule comprises a sequence having at least about 90% sequence identity to a molecule identified in SEQ ID NO: 1 (Figure 6).

8. (Previously Presented) The method of claim 1, wherein a methylated SPARC nucleic acid molecule comprises a sequence having at least about 95% sequence identity to a molecule identified in SEQ ID NO: 1 (Figure 6).

9. (Currently Amended) The method of claim 1, wherein the nucleic acid molecule is expressed at least at a lower level in a patient with cancer as compared to expression levels in a normal individual.

10. (Previously Presented) The method of claim 1, wherein the nucleic acid molecule is expressed at least about 5 fold lower in a patient with cancer as compared to expression in a normal individual.

11. (Previously Presented) The method of claim 1, wherein the nucleic acid molecule is expressed at least about 10 fold lower in a patient with cancer as compared to expression in a normal individual.

12. (Previously Presented) The method of claim 1 wherein the cancer is a pancreatic cancer.

13. (Previously Presented) The method of claim 1 wherein the subject sample is obtained from a mammalian patient.

14. (Previously Presented) The method of claim 1 wherein the subject sample is obtained from a human patient.

15. (Cancelled)

16. (Cancelled)

17. (Previously Presented) A method of claim 1 wherein the method of detecting a methylated SPARC nucleic acid comprising methylation specific polymerase chain reaction (MSP).

18. (Original) A method for detecting a methylated CpG-containing SPARC nucleic acid molecule comprising: contacting a nucleic acid-containing specimen with bisulfite to modify unmethylated cytosine to uracil; contacting the SPARC nucleic acid

molecule with oligonucleotide primers that discriminate between methylated and unmethylated CpGs; and detecting the methylated CpGs in the nucleic acid.

19. (Original) The method of claim 18, further comprising amplifying the CpG-containing nucleic acid in the specimen by means of the oligonucleotide primers.

20. (Original) The method of claim 19, wherein the amplifying step is the polymerase chain reaction (PCR).

21. (Original) The method of claim 18, wherein the CpG-containing nucleic acid is in a promoter region.

22. (Original) The method of claim 21, wherein the promoter is a tumor suppressor gene promoter.

23. (Original) The method of claim 18, wherein the specimen is from a tissue selected from the group consisting of pancreas, brain, colon, urogenital, lung, renal, hematopoietic, breast, thymus, testis, ovarian, and uterine.

24. (New) A method for diagnosing cancer, comprising the detection of a methylated SPARC nucleic acid molecule or a variant thereof in a sample from a subject, wherein the nucleic acid molecule is expressed at least about 5 fold lower in a patient with cancer as compared to expression in a normal individual.